


BLAST Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

[Edit](#) and [Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Blast 2 sequences

SEQ ID NO: 16-L27989

Results for: 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

|lcl|13245

Description

None

Molecule type

nucleic acid

Query Length

21

Subject ID

gij468333|gb|L27989.1|MSGRPOB

Description

Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB) gene, complete cds and RNA polymerase beta'-subunit rpoC gene, partial cds

Molecule type

nucleic acid

Subject Length

5084

Program

BLASTN 2.2.20+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

Search Parameters

Program	blastn
Word size	7
Expect value	1000
Hitlist size	100
Match/Mismatch scores	1,-3
Gapcosts	5,2
Filter string	F
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	1.37406	1.37406
K	0.710603	0.710603
H	1.30725	1.30725

Results Statistics

Effective search space 65988

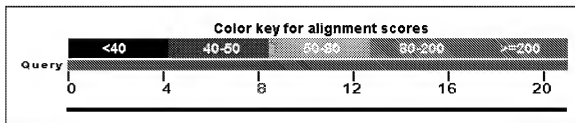
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Graphic Summary

Distribution of 14 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Plot of lcl|13245 vs gi|468333|gb|L27989.1|MSGRPOB [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

**Descriptions**

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

Sequence ID	Subject	Score	Length	Identity	E-value
L27989.1	Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB) gene, complete cds and RNA polymerase beta'-subunit rpoC gene, partial cds	28.2	228	100%	2e-04 100%

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Alignments [Select All](#) [Get selected sequences](#) [Distance tree of results](#)

>gb|L27989.1|MSGRPOB Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB)
gene, complete cds and RNA polymerase beta'-subunit rpoC gene,
partial cds
Length=5084

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Score = 28.2 bits (14), Expect = 2e-04
Identities = 21/22 (95%), Gaps = 1/22 (4%)
Strand=Plus/Minus

```
Query 1 CCATGAACACCG-CTGACTCTT 21
      |||
Sbjct 1527 CCATGAACACCGTCTGACTCTT 1506
```

Score = 22.3 bits (11), Expect = 0.013
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Minus

```
Query 11 CGCTGACTCTT 21
      |||
Sbjct 1940 CGCTGACTCTT 1930
```

Score = 16.4 bits (8), Expect = 0.79
Identities = 8/8 (100%), Gaps = 0/8 (0%)
Strand=Plus/Minus

```
Query 9 ACCGCTGA 16
      |||
Sbjct 949 ACCGCTGA 942
```

Score = 16.4 bits (8), Expect = 0.79
Identities = 8/8 (100%), Gaps = 0/8 (0%)
Strand=Plus/Plus

```
Query 4 TGAACACC 11
      |||
Sbjct 3811 TGAACACC 3818
```

Score = 16.4 bits (8), Expect = 0.79
Identities = 8/8 (100%), Gaps = 0/8 (0%)
Strand=Plus/Minus

```
Query 5 GAACACCG 12
      |||
Sbjct 3992 GAACACCG 3985
```

Score = 14.4 bits (7), Expect = 3.1
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Minus

```
Query 8 CACCGCT 14
      |||
Sbjct 307 CACCGCT 301
```

Score = 14.4 bits (7), Expect = 3.1
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Plus

Query 8 CACCGCT 14
 |||||
 Sbjct 1029 CACCGCT 1035

Score = 14.4 bits (7), Expect = 3.1
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Plus

Query 6 AACACCG 12
 |||||
 Sbjct 1491 AACACCG 1497

Score = 14.4 bits (7), Expect = 3.1
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Plus

Query 6 AACACCG 12
 |||||
 Sbjct 1860 AACACCG 1866

Score = 14.4 bits (7), Expect = 3.1
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Plus

Query 11 CGCTGAC 17
 |||||
 Sbjct 2059 CGCTGAC 2065

Score = 14.4 bits (7), Expect = 3.1
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Plus

Query 7 ACACCGC 13
 |||||
 Sbjct 2301 ACACCGC 2307

Score = 14.4 bits (7), Expect = 3.1
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Minus

Query 1 CCATGAA 7
 |||||
 Sbjct 2385 CCATGAA 2379

Score = 14.4 bits (7), Expect = 3.1
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Plus

Query 3 ATGAACA 9
 |||||
 Sbjct 3837 ATGAACA 3843

Score = 14.4 bits (7), Expect = 3.1
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Minus

Query 9 ACCGCTG 15
 |||||
 Sbjct 4263 ACCGCTG 4257

Select All Get selected sequences Distance tree of results